

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 16, 2003, 16:51:22 : Search time 81: 8571 Seconds
(without alignments)
137.557 Million cell updates/sec

Title: US-09-856-070-18

Perfect score: 24

Sequence: 1 KFLIM 5

Scoring table:

RIGSUM62
Xgapop 10.0 / Xgapov 0.5
Ygapop 10.0 / Ygapext 0.5
Zgapop 6.0 / Zgapext 7.0
Delop 6.0 / Delext 7.0

Searches: 2185239 seqs, 112599959 residues

Total number of hits satisfying chosen parameters: 432478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame_p2n.model -DEV-xlp
-O/-Cyn2 -ZUSHPlo.spool/209856370/runtat_14012003_155833_1611/3PE_queryfasta_1_1542
-DB-N.Geneseq.101002 -GMI-lastlap -SUFFIX.rng -MINMATCH=0 -1-10464126
-LOOEXT=0 -UNITS-bits -START=1 -END=1 -MATPIX-biosum62 -TPANS-human40.cdi
-LIST=45 -DOALIGN=200 -THP_SCORE=ext -THP_MAX=100 -THP_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0986070.acrgn_1_1448 -runtat_14012003_155833_1611 -NCP0=6 -1CP0=3
-NO_XLPXY -NO_MMAPP -LARGEQUERY -NPS_SCORES=0 -WAI0 -LON0102 -DEV_TMP001=120
-WAPN_TIME=01:30 -THPEAS=1 -X-AP-P=10 -X-AP-EXT=0.5 -P-AP-P=6 -EXTAPEXT=7
-YCAP-P=10 -YAPEXT=0.5 -DEL01=0.5 -DELEXT=7

Database : NCGeneseq.101002:*

1: /SUS22/3qcdat/a/geneseq/geneseq-emb1/NA1989.DAT:*

2: /SUS22/3qcdat/a/geneseq/geneseq-emb1/NA1989.DAT:*

3: /SUS22/3qcdat/a/geneseq/geneseq-emb1/NA1989.DAT:*

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22: /SUS22/3qcdat/a/geneseq/geneseq-emb1/NA1989.DAT:*

23: /SUS22/3qcdat/a/geneseq/geneseq-emb1/NA1989.DAT:*

24: /SUS22/3qcdat/a/geneseq/geneseq-emb1/NA1989.DAT:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	24	100.0	29	AA010529	Human WWF1 chimera
C 2	24	100.0	22	AA010529	Human homolog of D
C 3	24	100.0	34	AA010529	TEK (tetraacycline
4	24	100.0	51	AA010529	Human SNP oligonuc
5	24	100.0	56	AA010529	Glutathione-S-tran
6	24	100.0	60	AA010529	GLA469 Synthetic o
C 7	24	100.0	62	AA010529	CE3468 Synthetic o
C 8	24	100.0	77	AA010529	Bacillus adapted t
9	24	100.0	90	AA010529	Human breast cell
10	24	100.0	90	AA010529	Human fetal liver
11	24	100.0	90	AA010529	Probe #14080 for q
12	24	100.0	90	AA010529	Human brain expres
13	24	100.0	90	AA010529	Human bone marrow
14	24	100.0	90	AA010529	Probe #13465 for q
15	24	100.0	90	AA010529	Probe #17535 used
16	24	100.0	90	AA010529	Probe #17535 used t
17	24	100.0	90	AA010529	Human genome deriv
18	24	100.0	138	AA010529	Human secreted pro
19	24	100.0	140	AA010529	Human secreted pro
C 20	24	100.0	152	AA010529	DNA cassette eleme
21	24	100.0	150	AA010529	Aradopsis thalia
22	24	100.0	201	AA010529	Human immune/hacma
23	24	100.0	201	AA010529	Human immune/hacma
C 24	24	100.0	206	AA010529	Human secreted pro
25	24	100.0	220	AA010529	Nucleotide seque
26	24	100.0	223	AA010529	Corn tassol derive
27	24	100.0	249	AA010529	Nucleotide seque
28	24	100.0	251	AA010529	Nucleotide seque
29	24	100.0	270	AA010529	Human 36X polyu
30	24	100.0	301	AA010529	Human breast cell
31	24	100.0	301	AA010529	Human foetal liver
32	24	100.0	301	AA010529	Probe #13843 for q
33	24	100.0	301	AA010529	Human brain expres
34	24	100.0	301	AA010529	Human bone marrow
35	24	100.0	301	AA010529	Probe #13206 for q
36	24	100.0	301	AA010529	Probe #17278 used
37	24	100.0	301	AA010529	Probe #17278 used t
38	24	100.0	301	AA010529	Human genome deriv
C 39	24	100.0	301	AA010529	Human pancreatic c
40	24	100.0	320	AA010529	Human ovarian and
41	24	100.0	320	AA010529	Human cardiovascular
42	24	100.0	320	AA010529	Human reproductive
43	24	100.0	320	AA010529	Human digestive sy
44	24	100.0	320	AA010529	Human cardiovascular
45	24	100.0	320	AA010529	Human 36X polyu

ALIGNMENTS

RESULT 1
AA010529/C
10 AA010529 standard, DNA, 20 BP.
XX AA010529;
XX AA010529;
XX 24 SEP 2001 (first entry)
XX Human WWF1 chimera antisense oligonucleotide, ISLs #105026.
XX Human, ubiquitin protein ligase, WWF1, antitumour, antinflammatory,
XX (hepaty, inflammatory, inflammatory, human, chimera); antisense;
XX (hepaty, inflammatory, inflammatory, human, chimera); antisense;
XX Homo sapiens.
XX Synthetic.
FH Key Location/Qualifiers

modified_base 1..20
 /mod_base- a
 /note- "phosphorothioate backbone"
 modified_base 1..5
 /mod_base- b
 /note- "Methoxyethyl residues"
 modified_base 3
 /mod_base- c
 /mod_base- m5c
 modified_base 6
 /mod_base- d
 /mod_base- m5c
 misc_feature 6..15
 /mod_base- e
 /note- "Central gap region"
 modified_base 9
 /mod_base- f
 /mod_base- m5c
 modified_base 11
 /mod_base- g
 /mod_base- m5c
 modified_base 14
 /mod_base- h
 /mod_base- m5c
 modified_base 16..20
 /mod_base- i
 /note- "Methoxyethyl residues"
 modified_base 18
 /mod_base- j
 /mod_base- m5c
 modified_base 19
 /mod_base- k
 /mod_base- m5c
 modified_base 20
 /mod_base- l
 /mod_base- m5c
 US6258601-B1.
 10 JUL 2001.
 07-SEP-2000: 2000US-0657481
 07 SEP 2000: 2000US-0657481.
 (ISIS) ISIS PHARM INC.
 Monia BP, Cowest LM;
 WPI: 2001 450375/48.
 Antisense compounds capable of modulating expression of ubiquitin protein ligases WWP1 and WWP2, useful for diagnostic, prophylaxis and treatment of diseases e.g. infection, inflammation or tumors -
 Claim 3: Column 45-46; 47pp; English.
 The present invention relates to compounds, particularly antisense oligonucleotides, which are targeted to nucleic acids encoding ubiquitin protein ligases WWP1 and WWP2. The antisense oligonucleotides modulate the expression of WWP1 and WWP2. The antisense oligonucleotides WWP1 and WWP2 in cells or tissues in vitro. The oligonucleotides are useful for diagnosing, treating diseases associated with the expression of ubiquitin protein ligases WWP1 and WWP2 and for prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation and as a research reagent. The present sequence is a chimeric antisense oligonucleotide with a phosphorothioate backbone which inhibits human ubiquitin protein ligase WWP1 DNA expression.

SQ Sequence 20 BP; 4 A; 8 C; 0 G; 8 T; 0 other;
 Alignment Scores:
 Pred. No.: 39.5 Length: 20
 Score: 24.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-856-070-18 (1..5) x AAC19529 (1..20)
 QY 1 LysGluGluLeuMet 5
 DB 17 AACACAGTGAIG 3
 RESULT 2
 AAC90425/c
 ID AAC90425 standard; DNA: 22 BP.
 XX AC AAC90425;
 XX 19-MAR-2001 (first entry)
 XX Human homolog of Drosophila suppressor of deltex PCR primer #2.
 XX Human, angiogenesis, cancer, Drosophila suppressor of deltex; Su(dx);
 KW CADASIL; wound healing; rheumatoid arthritis; vascular disease;
 KW arteriosclerosis, PCR primer; ss.
 XX Homo sapiens.
 XX WO200073329-A2.
 XX 07-DEC-2000.
 XX 25-MAY-2000; 2000WO-0801990.
 XX 26-MAY-1999; 99CH-0012132.
 XX (UYMA-) UNIV VICTORIA MANCHESTER.
 XX Baron M;
 XX WPI: 2001-061509/07.
 XX Use of homologs of Drosophila Notch regulator gene and encoded protein products and antibodies in diagnosis and therapy of breast cancer.
 PT angiogenesis and diseases associated with abnormal notch signalling
 XX Examples: Page 33; 44pp; English.
 XX The present invention relates to a human homolog of Drosophila suppressor of deltex (Su(dx)) coding sequence and protein (AAC90425 and AAC50049). The human homologs are useful for in vitro diagnosis or therapy of diseases such as angiogenesis, colon cancer, cervical cancer, breast cancer, squamous adenocarcinoma, sarcoma, melanoma, lung cancer, dementia, cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL), wound healing, rheumatoid arthritis, vascular diseases such as arteriosclerosis. The present sequence is a PCR primer for the human homolog of Drosophila suppressor of deltex.
 XX SQ Sequence 22 BP; 4 A; 9 C; 1 G; 8 T; 0 other;
 Alignment Scores:
 Pred. No.: 43.9 Length: 22
 Score: 24.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-856-070-18 (1-5) x AAGGAGGAGTTCATG 5 (1-22)

QY 1 LysGlutLeuMet 5

DB 19 AAGGAGGAGTTCATG 5

RESULT 3

AAZ32614

ID AAZ32614 standard: DNA: 34 BP.

XX

AC AAZ32614:

XX

DE 19-JAN-2000 (first entry)

XX

DE TetR (Tetracycline repressor) gene 5' PCR primer.

XX

XX

KW Tetracycline: repressor; TetR; constitutive; plasmid; fusion gene;

KW cmtC; gram positive; replicon; inducible; expression; promoter;

KW operator; characterisation; PCR; primer; ss.

XX

OS Synthetic.

XX

PN W09953079-A1

XX

PD 21-OCT-1999.

XX

PF 14-APR-1999: G060-NS08155

XX

PR 14-APR-1998: 98US-0091753.

PR

PR 18-MAY-1998: 98US-0094844.

PR

PR 19-JUN-1998: 98US-0099828.

PR

PR 30-JUL-1998: 98US-0094638.

PR

PR 14-SEP-1998: 98US-0108211.

PR

PR 24-SEP-1998: 98US-0101718.

PR

PR 10-NOV-1998: 98US-0107751.

PR

PR 08-JAN-1999: 98US-0227687.

PR

PR 05-MAR-1999: 99US-0122949.

XX

PA (CUBI-) CUBIST PHARM INC.

XX

PI Tally FP, Tao J, Shen X, Zhang J.

XX

DR WPI: 1999-620437/53.

XX

PT New nucleic acid replicons for Gram-positive bacteria, used for

PT production of gene products of interest, e.g. for developing

PT antibiotics.

XX

XX

PS Example 1; Page 18: 60pp; English.

XX

CC This sequence represents a TetR (tetracycline repressor) 5' PCR

SCORC: 24.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 20

US-09-856-070-18 (1-5) x AAZ32614 (1-34)

QY 1 LysGlutLeuMet 5

DB 12 AAGGAGGAGTTCATG 26

RESULT 4

AAZ32614

ID AAZ32614 standard: DNA: 51 BP.

XX

AC AAZ32614:

XX

DE 24-JAN-2002 (first entry)

XX

DE Human SNP oligonucleotide #426.

XX

XX

KW Immunosuppressive; immunostimulatory; anti-inflammatory; cytostatic;

KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;

KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;

KW cyclin; polynucleotide; oncogene; histone; kinase; colony stimulating factor;

KW complement related protein; cytokine; kinase; cytokine; interferon;

KW interleukin; G-protein coupled receptor; thioesterase; inflammation;

KW multifactorial disease; autoimmune disease; infection;

KW nervous system disease; ss.

XX

OS Homo sapiens.

XX

PN W020047944-A2.

XX

PD 05-JUL-2001.

XX

PF 28-DEC-2000: 2000WO-US35498.

XX

PR 28-DEC-1999: 99US-0173419.

PR

PR 27-DEC-1999: 2000US-0173419.

PR

DR WPI: 2001-465210/50.

XX

XX

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polynucleotides,

PT oncogenes and histones, useful for diagnosing and treating, e.g.

PT cancer, autoimmune diseases and infections.

XX

PS Claim 1; Page 1513; 4143pp; English.

XX

CC The present invention relates to oligonucleotides encoding polymorphic

CC variants of proteins related to amylases, amyloid proteins, angiopoietin,

CC apoptosis related proteins, cadherin, cyclin, polynucleotide, oncogenes,

CC histone, kinase, colony stimulating factors, complement related

CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,

CC G protein coupled receptors and thioesterases, the present sequence is

CC one such oligonucleotide. The oligonucleotides and the peptides encoded

CC by them may be used in the prevention, diagnosis and treatment of

CC diseases associated with inappropriate expression of the proteins listed

CC above. Disorders that may be prevented, diagnosed and/or treated include

CC multifactorial diseases with a genetic component, such as autoimmune

QY 1 LysGlutLeuMet 5

DB 19 AAGGAGGAGTTCATG 5

RESULT 3

AAZ32614

ID AAZ32614 standard: DNA: 34 BP.

XX

AC AAZ32614:

XX

DE 19-JAN-2000 (first entry)

XX

DE TetR (Tetracycline repressor) gene 5' PCR primer.

XX

XX

KW Tetracycline: repressor; TetR; constitutive; plasmid; fusion gene;

KW cmtC; gram positive; replicon; inducible; expression; promoter;

KW operator; characterisation; PCR; primer; ss.

XX

OS Synthetic.

XX

PN W09953079-A1

XX

PD 21-OCT-1999.

XX

PF 14-APR-1999: G060-NS08155

XX

PR 14-APR-1998: 98US-0091753.

PR

PR 18-MAY-1998: 98US-0094844.

PR

PR 19-JUN-1998: 98US-0099828.

PR

PR 30-JUL-1998: 98US-0094638.

PR

PR 14-SEP-1998: 98US-0108211.

PR

PR 24-SEP-1998: 98US-0101718.

PR

PR 10-NOV-1998: 98US-0107751.

PR

PR 08-JAN-1999: 98US-0227687.

PR

PR 05-MAR-1999: 99US-0122949.

XX

PA (CUBI-) CUBIST PHARM INC.

XX

PI Tally FP, Tao J, Shen X, Zhang J.

XX

DR WPI: 1999-620437/53.

XX

PT New nucleic acid replicons for Gram-positive bacteria, used for

PT production of gene products of interest, e.g. for developing

PT antibiotics.

XX

XX

PS Example 1; Page 18: 60pp; English.

XX

CC This sequence represents a TetR (tetracycline repressor) 5' PCR

QY 1 LysGlutLeuMet 5

DB 19 AAGGAGGAGTTCATG 5

RESULT 3

AAZ32614

ID AAZ32614 standard: DNA: 34 BP.

XX

AC AAZ32614:

XX

DE 19-JAN-2000 (first entry)

XX

DE TetR (Tetracycline repressor) gene 5' PCR primer.

XX

XX

KW Tetracycline: repressor; TetR; constitutive; plasmid; fusion gene;

KW cmtC; gram positive; replicon; inducible; expression; promoter;

KW operator; characterisation; PCR; primer; ss.

XX

OS Synthetic.

XX

PN W09953079-A1

XX

PD 21-OCT-1999.

XX

PF 14-APR-1999: G060-NS08155

XX

PR 14-APR-1998: 98US-0091753.

PR

PR 18-MAY-1998: 98US-0094844.

PR

PR 19-JUN-1998: 98US-0099828.

PR

PR 30-JUL-1998: 98US-0094638.

PR

PR 14-SEP-1998: 98US-0108211.

PR

PR 24-SEP-1998: 98US-0101718.

PR

PR 10-NOV-1998: 98US-0107751.

PR

PR 08-JAN-1999: 98US-0227687.

PR

PR 05-MAR-1999: 99US-0122949.

XX

PA (CUBI-) CUBIST PHARM INC.

XX

PI Tally FP, Tao J, Shen X, Zhang J.

XX

DR WPI: 1999-620437/53.

XX

PT New nucleic acid replicons for Gram-positive bacteria, used for

PT production of gene products of interest, e.g. for developing

PT antibiotics.

XX

XX

PS Example 1; Page 18: 60pp; English.

XX

CC This sequence represents a TetR (tetracycline repressor) 5' PCR

QY 1 LysGlutLeuMet 5

DB 19 AAGGAGGAGTTCATG 5

RESULT 3

AAZ32614

ID AAZ32614 standard: DNA: 34 BP.

XX

AC AAZ32614:

XX

DE 19-JAN-2000 (first entry)

XX

DE TetR (Tetracycline repressor) gene 5' PCR primer.

XX

XX

KW Tetracycline: repressor; TetR; constitutive; plasmid; fusion gene;

KW cmtC; gram positive; replicon; inducible; expression; promoter;

KW operator; characterisation; PCR; primer; ss.

XX

OS Synthetic.

XX

PN W09953079-A1

XX

PD 21-OCT-1999.

XX

PF 14-APR-1999: G060-NS08155

XX

PR 14-APR-1998: 98US-0091753.

PR

PR 18-MAY-1998: 98US-0094844.

PR

Alignment Scores:
Pred. No.: 110 Length: 51
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-856-070-18 (1-5) x AAZ27218 (1-51)

QY 1 LysGlulIleuMet 5
DB 30 AAGGAAGGAAATTAATG 44

RESULT 5

AAZ42626

10 AAZ42626 standard; DNA: 56 BP.

XX

AC AAZ42626:

XX 19 JAN 2000 (first entry)

DE Glutathione-S-transferase PCR primer #2-5'-GSI(10etK).

XX Tetracycline; repressor; TetR; constitutive; plasmid; fusion gene;

KW Gram positive; replicon; inducible; expression; promoter; operator;

KW glutathione-S-transferase; GSI; characterisation; PCR; primer; ss.

XX Synthetic.

XX W09954079-A1.

XX 21-OCT-1999.

XX 14-APR-1999; 99W0-0508155.

XX 14-APR-1998; 98US-0081754.

XX 18-MAY-1998; 98US-0085844.

XX 19-JUN-1998; 98US-0089828.

XX 30-JUL-1998; 98US-0094698.

XX 14-SEP-1998; 98US-0100211.

XX 24-SEP-1998; 98US-0101718.

XX 10-NOV-1998; 98US-0107751.

XX 08-JAN-1999; 99US-0227687.

XX 05-MAR-1999; 99US-0122949.

XX (CUBI-) CUBIST PHARM INC.

XX Tally IP, Tao J, Shen X, Zhang J.

XX WPI: 1999-420437/53.

XX New nucleic acid replicons for Gram-positive bacteria, used for

PT production of gene products of interest, e.g. for developing

PT antibiotics.

XX Example 2; Page 22; 69pp; English.

XX This sequence represents a glutathione-S transferase (GST) PCR primer,

CC #2-5'-GSI(TetP) used with primer 3'-GSI(TetP) (AAZ42626) to amplify a

CC GST gene from plasmid pGEX-4T-2. The GST gene was then used in the

CC construction of a variety of novel nucleic acid replicons for

CC Gram positive bacteria comprising a gene of interest (GSI) under the

CC control of a tetracycline-inducible promoter/operator region. Such

CC replicons were transformed into a strain of *Staphylococcus aureus* which

CC constitutively expresses the tet repressor (TetR) in order to

CC characterise gene expression. The replicons can be used for high-level,

CC inducible production of a gene product in Gram-positive bacteria. The

CC gene expression is tightly repressed in the absence of tetracycline or

CC an analogue of tetracycline. The systems can be used for the production

CC of or analysis of the effects of gene products that may be toxic to the

CC host cells. They can also be used for testing a polypeptide for a

CC phenotypic effect on bacterial cells. They can also be used in test

CC animals for testing a fusion polypeptide for inhibition of growth of

CC bacterial cells, for developing antibiotics.

XX Sequence 56 BP; 20 A; 6 C; 15 G; 15 T; 0 other;

SC Alignment Scores:

Pred. No.: 122 Length: 56

Score: 24.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 20 Gaps: 0

US-09-856-070-18 (1-5) x AAZ32626 (1-56)

QY 1 LysGlulIleuMet 5

DB 18 AAGGAGGAATTAATG 32

RESULT 6

AAZ89727

10 AAZ89727 standard; DNA: 60 BP.

XX

AC AAZ89727:

XX 19-OCT-1999 (first entry)

XX C10469 Synthetic oligonucleotide for PCR or cassette construction.

XX Primer; PCR; cassette construction; recombination; plasmid;

KW gene regulation; tetracycline; infection; microbe; ss.

XX Synthetic.

XX W09936554-A1.

XX 22-JUL-1999.

XX 12-JAN-1999; 99W0-0500371.

XX 16-JAN-1998; 98US-0071640.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Ford CW, Quinn CL;

XX WPI: 1999-444407/37.

XX Characterization of microbial genes, used for identifying genes

PT which are targets for inhibition by antibiotics

XX Disclosure; Page 29; 92pp; English.

XX This oligonucleotide can be used to construct a synthetic promoter

CC region that contains two diverging transcription initiation signals.

CC Oligonucleotides AAX89726 to AAX89730 plus AAX89732 are also used in the

CC production of the promoter.

CC This stage is part of the method for identifying microbial genes as

CC possible antimicrobial targets.

CC The methods can be used for identifying which microbial genes

CC are targets for inhibition by antibiotics. The microbes may be bacteria,

CC e.g. *Staphylococcus aureus* virus, lower eukaryotes or yeast.

XX Sequence 60 BP; 25 A; 7 C; 11 G; 17 T; 0 other;

SC Alignment Scores:

Pred. No.: 132 Length: 60

Score: 24.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 20 Gaps: 0

US-09-856-070-18 (1-5) x AAX89727 (1-60)

QY 1 LysGluGluLeuMet 5
 ID AAX89726 standard; DNA; 62 BP.
 DB 42 AAGGAGGAATTAAATG 56

RESULT 7

AAX89726/c
 ID AAX89726 standard; DNA; 62 BP.
 AC AAX89726;
 DT 19-OCT-1999 (first entry)

DE CLQ468 Synthetic oligonucleotide for PCR or cassette construction.
 KW primer, PCR, cassette construction; recombination; plasmid;
 KW gene regulation; tetracycline, infection; microbe; ss.
 XX Synthetic.

OS W09936554-A1.
 PN 22-JUL-1999.
 PD 12-JAN-1999; 99W0-050637L.
 PF 16-JAN-1998; 99US-0071640.

XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Ford CW, Quinn CL;
 XX WPI; 1999-444407/37.

XX Characterization of microbial genes, used for identifying genes
 XX which are targets for inhibition by antibiotics
 XX Disclosure; Page 29; 92pp; English.

XX This oligonucleotide can be used to construct a synthetic promoter
 CC region that contains two diverging transcription initiation signals.
 CC oligonucleotides AAX89727 to AAX89740 plus AAX89732 are also used in the
 CC production of the promoter.
 CC This stage is part of the method for identifying microbial genes as
 CC possible antimicrobial targets.
 CC The methods can be used for identifying which microbial genes
 CC are targets for inhibition by antibiotics. The microbes may be bacteria,
 CC e.g. Staphylococcus aureus virus, lower eukaryotes or yeast.

SQ Sequence 62 BP; 17 A, 12 C, 7 G, 26 T, 0 other;

Alignment Scores:
 Pred. No.: 136 Length: 62
 Score: 24.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-856-070-18 (1-5) x AAX89726 (1-62)

QY 1 LysGluGluLeuMet 5
 ID AAX89726 standard; DNA; 62 BP.
 DB 42 AAGGAGGAATTAAATG 56

RESULT 8

AAX11699/c
 ID AAX11699 standard; DNA; 77 BP.
 XX AAX11699;
 AC AAX11699;
 DT 19-JUN-1991 (first entry)

XX Bacillus adapted tetracycline repressor promoter sequence (MaxXX).
 DE Tetracycline repressor, tetP promoter, xylose isomerase promoter;
 KW tet operator; ds.
 XX Key Location/Qualifiers
 FT 33..51
 FT /*tag= a
 FT /label= tet-operator 01

XX DE3934454-A.
 XX 18-APR-1991.
 XX 14-OCT-1989; 89DR-3934454.
 XX 14 OCT-1989, 89DE-3934454.
 XX (MERE) MERCK PATENT GMBH.
 XX Hillen W, Geissendorfer M;
 XX WPI; 1991-118470/17.

XX Vector for inducible protein over-expression in Bacillus - has
 XX tetracycline repressor gene and its adapted promoter, xylose
 XX isomerase promoter and tetracycline operator sequence
 XX Disclosure; fig 8; 16pp; German.

XX This is a tetracycline repressor (tetR) promoter sequence, MaxXX which
 CC has been adapted for expression in Bacillus cells. It is a fragment of
 CC the regulatable expression vectors pW4350, -352 and -353. In the
 CC latter it is linked to a 2nd adapted xylose-isomerase resistance
 CC promoter (xylP). It is used in the construction of the regulatable
 CC expression vectors pW4353 and pW4354 which comprise (a) the tetracycline
 CC repressor gene (tetR); (b) this Bacillus adapted tetP-promoter sequence;
 CC (c) an adapted xylose isomerase promoter sequence (xylP); and (d) at
 CC least one tet operator sequence (tetO) between the consensus regions of
 CC xylP. These constructs are used for inducible over expression of
 CC proteins in Bacillus hosts. The 5' end overhangs the 3' end of the
 CC complementary strand and the 5' end of the complementary strand
 CC overhangs the 3' end of this sense strand, by CIAG.
 XX See also AAX11697-98 and AAX11700.

XX SQ Sequence 77 BP; 14 A, 13 C, 4 G, 36 T, 0 other;

Alignment Scores:
 Pred. No.: 173 Length: 77
 Score: 24.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-856-070-18 (1-5) x AAX11699 (1-77)

QY 1 LysGluGluLeuMet 5
 ID AAX11699 standard; DNA; 77 BP.
 DB 23 AAGGAGGAATTAAATG 9

RESULT 9

AHA50681
 ID AHA50681 standard; DNA; 90 BP.
 XX AHA50681;
 AC AHA50681;
 DT 01-FEB-2002 (first entry)

XX Human breast cell single exon nucleic acid probe #9376.
 DE Human, microarray, single exon probe, gene expression; breast;
 KW

KW disease; cancer; ss.
 XX Homo sapiens.
 XX W0200157271 A2.
 XX 09-AUG-2001
 XX 30-JAN-2001; 2001WO-0500662.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0632366.
 XX 21-SEP-2000; 2000US-0234587.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000US-0234263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR.
 XX WPI: 2001-496943/54
 XX New spatially-addressable set of single exon nucleic acid probes,
 XX useful for measuring gene expression in sample derived from human
 XX breast, comprises number of single exon nucleic acid probes
 XX Claim 4: SEQ ID NO 9376; 327pp + sequence listing; English.
 XX The invention relates to a spatially addressable set of single exon
 XX nucleic acid probes for measuring gene expression in a sample derived
 XX from human breast and BT 474 cells. The method involves contacting
 XX the probes with a collection of detectably labelled nucleic acids
 XX derived from mRNA of human breast, and then measuring the label
 XX bound to each probe of the microarray. The probes are useful for
 XX verifying the expression of regions of genomic DNA predicted to
 XX encode proteins. They are useful for gene discovery, and for
 XX determining predisposition and/or prognosing breast disease. Gene
 XX expression analysis is useful for assessing the toxicity of chemical
 XX agents on cells. The microarray of this invention presents a far greater
 XX diversity of probes for measuring gene expression, with far less bias
 XX than expressed sequence tag microarrays. The method is suitable for
 XX rapid production of functional information from genomic sequence. The
 XX present sequence is a single exon nucleic acid probe of the invention
 XX Note: The sequence data for this patent did not form part of the
 XX printed specification, but was obtained in electronic format directly
 XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 90 BP; 36 A; 17 C; 18 G; 19 T; 0 other;
 Alignment Scores:
 Pred. No.: 205 Length: 90
 Score: 24.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 US-09-856-070-18 (1-5) x AHA50681 (1-90)
 QY 1 LysGluGluLeuMet 5
 ID AHA35614 standard; DNA; 90 BP.
 AC AHA35614;
 XX 23-AUG-2002 (first entry)
 DE Probe #14080 for gene expression analysis in human heart cell sample.
 XX Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 XX congenital heart disease; ss.
 XX Homo sapiens.
 XX
 DE Human foetal liver single exon nucleic acid probe #16951.
 XX Human; foetal liver, gene expression, single exon nucleic acid probe; ss.
 XX Homo sapiens.
 XX W0200157277 A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-0500669.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0632366.
 XX 21-SEP-2000; 2000US-0234587.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000US-0234263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR.
 XX WPI: 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human foetal liver
 XX Claim 4: SEQ ID NO 16951; 639pp + sequence listing; English.
 XX The invention relates to a single exon nucleic acid probe for
 XX measuring human gene expression in a sample derived from human foetal
 XX liver. The single exon nucleic acid probes may be used for predicting,
 XX measuring and displaying gene expression in samples derived from human
 XX foetal liver. The present sequence is a single exon nucleic acid
 XX probe of the invention.
 XX Note: The sequence data for this patent did not form part of the
 XX printed specification, but was obtained in electronic format directly
 XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 90 BP; 36 A; 17 C; 18 G; 19 T; 0 other;
 Alignment Scores:
 Pred. No.: 205 Length: 90
 Score: 24.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 US-09-856-070-18 (1-5) x ABA68646 (1-90)
 QY 1 LysGluGluLeuMet 5
 ID ABA35614 standard; DNA; 90 BP.
 AC ABA35614;
 XX 23-AUG-2002 (first entry)
 DE Probe #14080 for gene expression analysis in human heart cell sample.
 XX Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 XX congenital heart disease; ss.
 XX Homo sapiens.
 XX

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PN WC200157274-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00666.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 04-AUG-2000; 2000US-0234687.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-488899/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX Claim 4: SEQ ID NO 14080, 530pp, English.
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and proposing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at http://wipo.int/pub/published-pat\_sequences
XX
XX Sequence 90 BP; 36 A; 17 C; 18 G; 19 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 205 Length: 90
XX Score: 24.00 Matches: 5
XX Percent Similarity: 100.00% Conservatives: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 22 Gaps: 0
XX
XX US-09-856-070-18 (1-5) x ARA5614 (1-90)
XX
XX QY 1 LysGluGluLeuMet 5
XX DB 23 AAAGAAGAGCTGATG 37
XX
XX RESULT 12
XX AAK1694
XX ID AAK16994 standard; DNA; 90 BP.
XX AC AAK16994;
XX DT 06-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 16985.
XX KW Human: brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer; ss.
XX OS Homo sapiens
XX PN WC200157275-A2
XX XX 04-AUG-2001

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XX 30-JAN-2001; 2001WO-US00667.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 04-AUG-2000; 2000US-0234687.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
XX Example 4: SEQ ID NO: 16985; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
XX Sequence 90 BP; 46 A; 17 C; 18 G; 19 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 205 Length: 90
XX Score: 24.00 Matches: 5
XX Percent Similarity: 100.00% Conservatives: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 22 Gaps: 0
XX
XX US-09-856-070-18 (1-5) x AAK1694 (1-90)
XX
XX QY 1 LysGluGluLeuMet 5
XX DB 23 AAAGAAGAGCTGATG 37
XX
XX RESULT 13
XX AAK42778
XX ID AAK42778 standard; DNA; 90 BP.
XX AC AAK42778;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 17335.
XX KW Human: bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens
XX PN WC200157276-A2.
XX XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00668.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 04-AUG-2000; 2000US-0234687.

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CC expression in samples derived from human placenta. the probes are useful
 CC for antenatal diagnosis of human genetic disorders.

XX
 SQ Sequence 90 BP: 36 A; 17 C; 18 G; 19 T; 0 other;

Alignment Scores:
 Pred. No.: 205 Length: 90
 Score: 24.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-856-070-18 (1-5) x AA148849 (1-90)

QY 1 LysGluGluLeuMet 5
 |||||
 DB 23 AAAGAACAGCTGATG 37

Search completed: January 16, 2003, 17:19:39
 Job time : 83.9821 secs

